

Serial No.: 09/745,965
Attorney Docket: 3373.1

AMENDMENTS

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Amendments to the Claims

This listing of claims will replace all prior versions, and listings, of claims in the application:

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1. (currently amended) A computer implemented method for selecting probes for gene expression monitoring comprising:

- a) predicting hybridization intensities of a plurality of candidate against a plurality of RNA transcripts and their corresponding control probes; and
- b) selecting the candidate probes that have the highest intensity difference over its their corresponding control probe probes.

2. (original) The method of Claim 1 wherein said hybridization intensity (I) is determined using the equation:

$$I = \exp\left[\sum_i P_i S_i\right]$$

wherein said P_i is the value of the i th parameter and S_i is a value derived from the sequence of said probe.

3. (original) The method of Claim 2 wherein said P_i is the free energy of a base in a given position of said sequence relative to a reference base selected from the group consisting of A, C, G and T.

Serial No.: 09/745,965
Attorney Docket: 3373.1

4. (previously presented) The method of Claim 3 wherein said Si is a functional of said sequence.
5. (previously presented) The method of Claim 3 wherein said Pi is determined empirically.
6. (original) The method of Claim 5 wherein said Pi is determined by least square fit using a training data set.
7. (original) The method of Claim 5 wherein Pi is determined using Cholesky decomposition.
8. (original) The method of Claim 7 wherein said Si for a given nucleotide type is replaced with a smooth function of probe base number.
9. (original) The method of Claim 8 wherein said smooth function is a polynomial function.
10. (original) The method of Claim 7 wherein said Si for a given nucleotide type is replaced with a smooth function of the difference of a base to the central position.
11. (original) The method of Claim 8 wherein said smooth function is a polynomial function.

Serial No.: 09/745,965
Attorney Docket: 3373.1

12. (original) The method of Claim 7 wherein said equation includes at least one parameter describing probe-probe hybridization.

13. (original) The method of Claim 7 wherein said equation includes at least one parameter describing hairpin formation.

14. (original) The method of Claim 7 wherein said equation includes parameters describing nearest neighbor interactions.

15. (original) The method of Claim 7 wherein said P_i is determined using singular value decomposition.

16 - 44 (canceled)

45. (currently amended) A computer software product for selecting probes for gene expression monitoring comprising:

computer program code for predicting hybridization intensities of a plurality of candidate probes and their corresponding control probes;

computer program code for selecting the candidate probes that have the highest intensity difference over ~~its corresponding control probe~~ their corresponding control probes; and

a computer readable media for storing said codes.

Serial No.: 09/745,965
Attorney Docket: 3373.1

46. (original) The computer software product of Claim 45 wherein said computer code for predicting hybridization intensity (I) comprising code for calculating using the equation:

$$I = \exp\left[\sum_i P_i S_i\right]$$

wherein said P_i is the value of the i th parameter and S_i is a value derived from the sequence of said probe.

47. (original) The computer software product of Claim 46 wherein said P_i is the free energy of a base in a given position of said sequence relative to a reference base selected from the group consisting of A, C, G and T.

48. (original) The computer software product of Claim 47 wherein said S_i is a functional of said sequence.

49. (original) The computer software product of Claim 47 wherein said P_i is determined empirically.

50. (original) The computer software product of Claim 49 wherein said P_i is determined by least square fit using a training data set.

51. (original) The computer software product of Claim 50 wherein P_i is determined using Cholesky decomposition.

Serial No.: 09/745,965
Attorney Docket: 3373.1

52. (original) The computer software product of Claim 51 wherein said S_i for a given nucleotide type is replaced with a smooth function of probe base number.

53. (original) The computer software product of Claim 52 whereon said smooth function is a polynomial function.

54. (original) The computer software product of Claim 52 wherein said S_i for a given nucleotide type is replaced with a smooth function of the difference of a base to the central position.

55. (original) The computer software product of Claim 52 wherein said smooth function is a polynomial function.

56. (original) The computer software product of Claim 51 wherein said equation includes at least one parameter describing probe-probe hybridization.

57. (original) The computer software product of Claim 51 wherein said equation includes at least one parameter describing hairpin formation.

58. (original) The computer software product of Claim 51 wherein said equation includes parameters describing nearest neighbor interactions.

59. (original) The computer software product of Claim 58 wherein said P_i is determined using singular value decomposition.